CLAIMS

1. A genetic marker, which exists in a genomic DNA of a Gramineae plant and is linked to a Fusarium head blight-resistance factor, wherein:

a distance from the Fusarium head blight-resistance factor to the Genetic marker is within a range of approximately 0 to 10cM.

2. The genetic marker as set forth in Claim 1, wherein the Gramineae plant is a Hordeum or Triticum.

3. The genetic marker as set forth in Claim 2, wherein the Hordeum or Triticum is barley.

4. The genetic marker as set forth in Claim 3, wherein the genomic DNA is 2H chromosome.

5. The genetic marker as set forth in any one of Claims 1 to 4, wherein the genetic marker is for being amplified with a first primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 1, and a primer having the base sequence of S.E.Q. ID. NO. 2.

6. The genetic marker as set forth in Claim 5, being distanced from the Fusarium head blight-resistance factor by approximately 0cM.

7. The genetic marker as set forth in any one of Claims 1 to 4, wherein the genetic marker is for being amplified with a second primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 3, and a primer having the

base sequence of S.E.Q. ID. NO. 4.

8. The genetic marker as set forth in Claim 7, being distanced from the Fusarium head blight-resistance factor by approximately 0.6cM.

9. The genetic marker as set forth in Claim 8, wherein the Genetic marker has the base sequence of S.E.Q. ID. NO. 8 or 9.

10. The genetic marker as set forth in any one of Claims 1 to 4, wherein the genetic marker is for being amplified with a sixth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 22, and a primer having the base sequence of S.E.Q. ID. NO. 23.

11. The genetic marker as set forth in any one of Claims 1 to 4, wherein the genetic marker is for being amplified with a seventh primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 24, and a primer having the base sequence of S.E.Q. ID. NO. 25.

12. The genetic marker as set forth in any one of Claims 1 to 4, wherein the genetic marker is for being amplified with an eighth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 26, and a primer having the base sequence of S.E.Q. ID. NO. 27.

13. (Amended) The genetic marker as set forth in Claim 3, wherein the genomic DNA is 5H chromosome.

14. The genetic marker as set forth in Claim 1, 2, or 13,

wherein the genetic marker is for being amplified with a third primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 5, and a primer having the base sequence of S.E.Q. ID. NO. 6.

15. The genetic marker as set forth in Claim 14, being distanced from the Fusarium head blight-resistance factor by approximately 9cM.

16. The genetic marker as set forth in Claim 15, wherein the genetic marker has the base sequence of S.E.Q. ID. NO. 10 or 11.

17. The genetic marker as set forth in Claim 1, 2, or 13, wherein the genetic marker is for being amplified with a fourth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 5, and a primer having the base sequence of S.E.Q. ID. NO. 7.

18. The genetic marker as set forth in Claim 17, being distanced from the Fusarium head blight-resistance factor by approximately 9cM.

19. The genetic marker as set forth in Claim 18, wherein the genetic marker has the base sequence of S.E.Q. ID. NO. 12 or 13.

20. The genetic marker as set forth in Claim 1, 2, 3, or 13, wherein:

amplification of the genetic marker is carried out by:

(a) ligating MseI adaptors having the base sequences of

S.E.Q. ID. NOs. 16 and 17 and EcoRI adaptors having the base sequences of S.E.Q. ID. NOs. 14 and 15 to a DNA fragment obtained by digesting a genomic DNA of a Gramineae plant with restriction enzymes MseI and EcoRI,

(b) performing pre-amplification of the ligated DNA fragment by using MseI universal primer having the base sequence of S.E.Q. ID. NO. 19, and EcoRI universal primer having the base sequence of S.E.Q. ID. NO. 18, and

(c) amplifying the pre-amplified fragment by using a fifth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 21, and a primer having the base sequence of S.E.Q. ID. NO. 20.

21. The genetic marker as set forth in Claim 13 or 20, being distanced from the Fusarium head blight-resistance factor by approximately 2.2cM.

22. The genetic marker as set forth in Claim 1, 2, 3, or 13, wherein the genetic marker is for being amplified with a ninth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 28, and a primer having the base sequence of S.E.Q. ID. NO. 29.

23. The genetic marker as set forth in Claim 1, 2, 3, or 13, wherein the genetic marker is for being amplified with a tenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 30, and a primer having the base sequence of S.E.Q. ID. NO. 31.

24. The genetic marker as set forth in Claim 3, wherein the genomic DNA is 4H chromosome.

25. (Amended) The genetic marker as set forth in Claim 1, 2, 3, or 24, wherein:

amplification of the genetic marker is carried out by

(a) ligating MseI adaptors having the base sequences of S.E.Q. ID. NOs. 16 and 17 and EcoRI adaptors having the base sequences of S.E.Q. ID. NOs. 14 and 15 to a DNA fragment obtained by digesting a genomic DNA of a Gramineae plant with restriction enzymes MseI and EcoRI,

(b) performing pre-amplification of the ligated DNA fragment by using MseI universal primer having the base sequence of S.E.Q. ID. NO. 19, and EcoRI universal primer having the base sequence of S.E.Q. ID. NO. 18, and

(c) amplifying the pre-amplified fragment by using an eleventh primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 32, and a primer having the base sequence of S.E.Q. ID. NO. 33.

26. (Amended) The genetic marker as set forth in Claim 1, 2, 3, or 24, wherein:

amplification of the genetic marker is carried out by

(a) ligating MseI adaptors having the base sequences of S.E.Q. ID. NOs. 16 and 17 and EcoRI adaptors having the base sequences of S.E.Q. ID. NOs. 14 and 15 to a DNA fragment obtained by digesting a genomic DNA of a Gramineae plant with restriction enzymes MseI and EcoRI,

(b) performing pre-amplification of the ligated DNA fragment by using MseI universal primer having the base sequence of S.E.Q. ID. NO. 19, and EcoRI universal primer having the base sequence of S.E.Q. ID. NO. 18, and

(c) amplifying the pre-amplified fragment by using a

twelfth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 34, and a primer having the base sequence of S.E.Q. ID. NO. 35.

27. (Amended) The genetic marker as set forth in Claim 1, 2, 3, or 24, wherein:

amplification of the genetic marker is carried out by

(a) ligating MseI adaptors having the base sequences of S.E.Q. ID. NOs. 16 and 17 and EcoRI adaptors having the base sequences of S.E.Q. ID. NOs. 14 and 15 to a DNA fragment obtained by digesting a genomic DNA of a Gramineae plant with restriction enzymes MseI and EcoRI,

(b) performing pre-amplification of the ligated DNA fragment by using MseI universal primer having the base sequence of S.E.Q. ID. NO. 19, and EcoRI universal primer having the base sequence of S.E.Q. ID. NO. 18, and

(c) amplifying the pre-amplified fragment by using a thirteenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 36, and a primer having the base sequence of S.E.Q. ID. NO. 37.

28. (Amended) The genetic marker as set forth in Claim 1, 2, 3, or 24, wherein the genetic marker is for being amplified with a fourteenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 38, and a primer having the base sequence of S.E.Q. ID. NO. 39.

29. (Amended) The genetic marker as set forth in Claim 1, 2, 3, or 24, wherein the genetic marker is for being amplified with a fifteenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 40, and a primer

having the base sequence of S.E.Q. ID. NO. 41.

30. (Amended) The genetic marker as set forth in Claim 1, 2, 3, or 24, wherein the genetic marker is for being amplified with a sixteenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 42, and a primer having the base sequence of S.E.Q. ID. NO. 43.

31. The genetic marker as set forth in Claim 3, wherein the genomic DNA is 6H chromosome.

32. (Amended) The genetic marker as set forth in Claim 1, 2, 3, or 31, wherein:

amplification of the genetic marker is carried out by

(a) ligating MseI adaptors having the base sequences of S.E.Q. ID. NOs. 16 and 17 and EcoRI adaptors having the base sequences of S.E.Q. ID. NOs. 14 and 15 to a DNA fragment obtained by digesting a genomic DNA of a Gramineae plant with restriction enzymes MseI and EcoRI,

(b) performing pre-amplification of the ligated DNA fragment by using MseI universal primer having the base sequence of S.E.Q. ID. NO. 19, and EcoRI universal primer having the base sequence of S.E.Q. ID. NO. 18, and

(c) amplifying the pre-amplified fragment by using a seventeenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 44, and a primer having the base sequence of S.E.Q. ID. NO. 45.

33. The genetic marker as set forth in Claim 1, 2, 3, or 31, wherein the genetic marker is for being amplified with an eighteenth primer set that is a combination of a primer having

the base sequence of S.E.Q. ID. NO. 46, and a primer having the base sequence of S.E.Q. ID. NO. 47.

34. A DNA fragment isolating method, comprising:

isolating, by using the genetic marker as set forth in any one of Claims 1 to 33, a DNA fragment including a Fusarium head blight-resistance factor.

35. A method for producing a Fusarium head blight-resistance plant, comprising:

introducing, into a genomic DNA of a plant, the DNA fragment that is obtained by the method as set forth in Claim 34 and includes the Fusarium head blight-resistance factor.

36. The genetic marker as set forth in Claim 35, wherein the plant is Gramineae.

37. The genetic marker as set forth in Claim 36, wherein the Gramineae plant is Hordeum or Triticum.

38. The genetic marker as set forth in Claim 37, wherein the Hordeum or Triticum is barley.

39. A Fusarium head blight-resistant plant obtained by the method as set forth in any one of Claims 35 to 38.

40. A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

detecting the genetic marker as set forth in any one of Claims 1 to 33.

41. A kit for judging, by the method as set forth in Claim 40, whether a plant is a Fusarium head blight-resistant plant or not.

42. A gene detecting apparatus, wherein at least one of the genetic markers as set forth in Claims 1 to 33 is fixed.

43. A primer population for use in detecting the genetic markers as set forth in Claims 1 to 33, comprising:

at least two of primers having the base sequences of S.E.Q. ID. NOs. 1 to 7, and 20 to 47.

44. (New) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic markers as set forth in Claims 5 and 7, respectively.

45.(New) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic markers as set forth in Claims 11 and 12, respectively.

46.(New) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of a polymorphism of the genetic marker as set forth in Claim 14 or 17, and a polymorphism of the genetic marker as set forth in Claim 20.

47.(New) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic

markers as set forth in Claims 22 and 23, respectively.

48.(New) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic markers as set forth in Claims 25 and 26, respectively.

49.(New) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic markers as set forth in Claims 27 and 28, respectively.

50.(New) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic markers as set forth in Claims 29 and 30, respectively.

51.(New) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic markers as set forth in Claims 32 and 33, respectively.

52.(New) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic markers as set forth in Claims 7 and 10, respectively.